The MaRS (Matrix of RNA-Seq) Project

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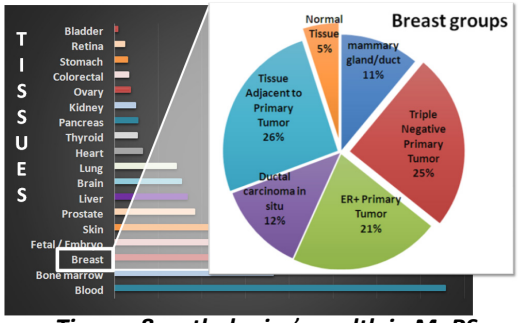
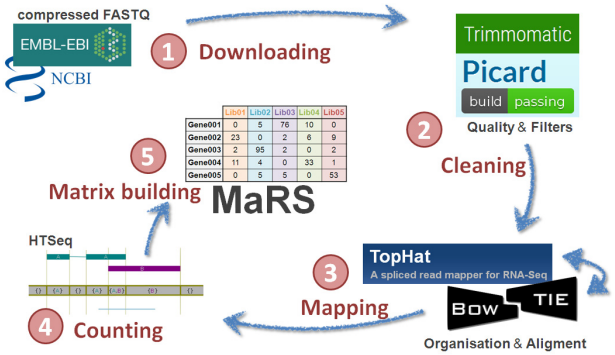
Recent years have seen a dramatic **increase** in the **amount** of genomic and **transcriptomic data** produced by laboratories around the world. The aim of the **MaRS research program** is to **collect** and to allow the **comparison** of these data. MaRS is focused on the **RNA-Seq** method, which reflects the expression of the genes in a specific condition.



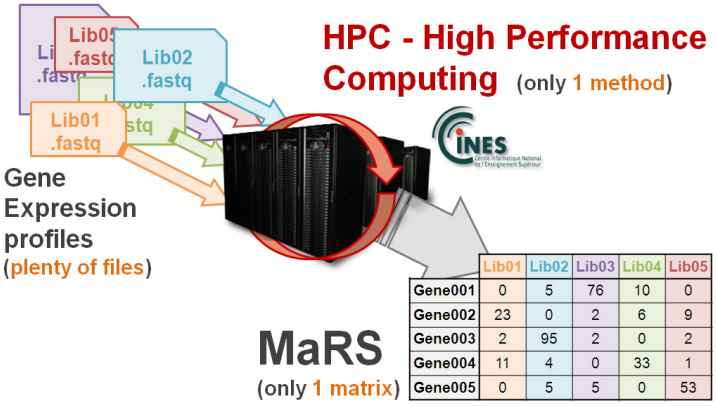
Tissues & pathologies' wealth in MaRS

27000 Human RNA-Seq profiles are selected for the project. In collaboration with the CINES, all these data are **collected** and **computed** with a single **method** to allow their **compilation** in **one matrix**: MaRS.
It represents a **huge amount of data** and requires the use of High performance computing (**HPC**) on the cluster ***Occigen*** (CINES): 120 To of compressed data downloaded and 1.2 million hours/core consumed.



High Performance Computing toolchain

RNA-Seq method is used in a wide variety of applications like identifying **disease-related** genes, analysing the effects of drugs on **tissues** or providing insight into disease pathways. The RNA-Seq is widely used to identify **gene expression patterns** associated with tumor formation.
MaRS represents a fantastic tool for the discovery and the validation of **Biomarkers**.



The MaRS project

Many **challenges** were encountered and solved during the project:
- the **download** of the very large amount of data
- the **installation** and the **settings** of the software's in the cluster
- the **optimization** of the compiler and the packages
- the **constraints** in jobs duration and jobs limitations.

➔Next? The Exploration of MaRS! Implementation of an advanced search tool to query the matrix in order to highlight biomarkers.
➔Extend work to other species: Mouse.

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